



SEQUENCE LISTING

<110> Zhou, Shibin
Zawel, Leigh
Vogelstein, Bert
Kinzler, Kenneth

<120> Human Fast-1 Gene

<130> 01107.10898

<140> 09/113,309

<141> 1998-07-10

<160> 19

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1793

<212> DNA

<213> Homo sapiens

<400> 1

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agcagctgct	agatcctgaa	ctccaggagc	gccccacgcc	ttgggagctt	ggcatgggct	180
aaataactccc	ccatttgta	aatgggggtcc	tgaaacctga	ccagggaaga	cgggataaag	240
tagccatggg	tcatgcgagc	ccctttgaag	ccgggectgg	ccacccaaag	gcaactcagg	300
ggtggagact	gaggcctcag	gagaagcccc	cactagaatg	ctctctgccc	ctcccttcca	360
gattaaccaa	aacctgctaa	ttgtggaagc	cctcggcatg	ctccccctcc	ccacagcctc	420
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ccagcccggc	ctcaggtccc	ggccctgcct	tctacactgc	cccaccgccc	tgcacctctc	540
acccggccag	gccccctgcc	acgctgtcta	ccgtcccgcga	tggggccctg	cagcgggtcc	600
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gcccgtccct	cccgagact	gaagctggcc	cagatcatcc	gtcagggtcca	ggccgtgttc	780
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aaaccgatgct	tccgcaaggt	gcccgaaggac	cctgcaaagc	cccaggccaa	gggcaacttc	900
tggggcggtcg	acgtgagcct	gatcccagct	gaggcgctcc	ggctgcagaa	caccgcctcg	960
tgccggcgct	ggcagaacgg	aggtgcgcgt	ggagccttcg	ccaaggacct	gggcccctac	1020
gtgctgcacg	gcccggccata	ccggccgccc	agtccccccg	caccacccag	tgagggtctc	1080
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cagagcagcc	cagttcctgc	aggcacaggg	aacagtgggg	aggaggcggt	gcccacccca	1200
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aatgtggtaa	tgcccttggc	accaccaccc	acctcctgtc	cccagtgtcc	gtcaaccagc	1500
cctgcctact	gggggggtgg	ccctgaaacc	cgaggggcccc	cagggctgct	ctgcgatcta	1560
gacgccctct	tccaaggggt	gccacccaac	aaaagcatct	acgacgtttg	ggtcagccac	1620
cctcgggacc	tggcgggccc	tggcccaggc	tggctgctct	cctggtgcag	cctgtgaggg	1680
tcttaagaca	ggggccgctc	ctccctcccg	ctcccacccc	caccttgttg	acagggagca	1740
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<210> 2

<211> 365

COPY

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Pro Cys Ser Gly Ser Arg Leu Gly Pro Pro Glu Ala Glu Ser
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Pro Ser Gln Pro Pro Lys Arg Arg Lys Arg Tyr Leu Arg His Asp
20 25 30
Lys Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala
35 40 45
Ala Pro Ser Arg Arg Leu Lys Leu Ala Gln Ile Ile Arg Gln Val Gln
50 55 60
Ala Val Phe Pro Phe Phe Arg Glu Asp Tyr Glu Gly Trp Lys Asp Ser
65 70 75 80
Ile Arg His Asn Leu Ser Ser Asn Arg Cys Phe Arg Lys Val Pro Lys
85 90 95
Asp Pro Ala Lys Pro Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val
100 105 110
Ser Leu Ile Pro Ala Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys
115 120 125
Arg Arg Trp Gln Asn Gly Gly Ala Arg Gly Ala Phe Ala Lys Asp Leu
130 135 140
Gly Pro Tyr Val Leu His Gly Arg Pro Tyr Arg Pro Pro Ser Pro Pro
145 150 155 160
Pro Pro Pro Ser Glu Gly Phe Ser Ile Lys Ser Leu Leu Gly Gly Ser
165 170 175
Gly Glu Gly Ala Pro Trp Pro Gly Leu Ala Pro Gln Ser Ser Pro Val
180 185 190
Pro Ala Gly Thr Gly Asn Ser Gly Glu Glu Ala Val Pro Thr Pro Pro
195 200 205
Leu Pro Ser Ser Glu Arg Pro Leu Trp Pro Leu Cys Pro Leu Pro Gly
210 215 220
Pro Thr Arg Val Glu Gly Glu Thr Val Gln Gly Gly Ala Ile Gly Pro
225 230 235 240
Ser Thr Leu Ser Pro Glu Pro Arg Ala Trp Pro Leu His Leu Leu Gln
245 250 255
Gly Thr Ala Val Pro Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser
260 265 270
Leu Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn
275 280 285
Val Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro
290 295 300
Ser Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro
305 310 315 320
Pro Gly Leu Leu Cys Asp Leu Asp Ala Leu Phe Gln Gly Val Pro Pro
325 330 335
Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala
340 345 350
Ala Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu
355 360 365

<210> 3

<211> 477

<212> PRT

<213> Homo sapiens

<400> 3

Val Ala Met Ile Asn Ala Cys Ile Asp Ser Met Ser Ser Ile Leu Pro
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Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys Ser Ala
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Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu Gln Asn Gly Gln Glu Glu
35 40 45
Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys
50 55 60
Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Cys
65 70 75 80
Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile Trp Gly
85 90 95
Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly Leu Tyr
100 105 110
Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln Val Ser
115 120 125
His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp Arg Trp
130 135 140
Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn Cys Glu
145 150 155 160
Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His
165 170 175
Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg
180 185 190
His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr Thr His
195 200 205
Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser
210 215 220
Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu Asp Gly
225 230 235 240
Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly Ser Pro
245 250 255
Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser Leu Asp
260 265 270
Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser Ile Ala
275 280 285
Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln
290 295 300
Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg
305 310 315 320
Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr Val Glu
325 330 335
Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly
340 345 350
Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln
355 360 365
Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys
370 375 380
Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe
385 390 395 400
Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr
405 410 415
Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp
420 425 430
Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile
435 440 445
Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr
450 455 460
Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
465 470 475

<210> 4
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 <212> DNA
 <213> Homo sapiens

 <400> 4
 tgtkkatt 8

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 <211> 18
 <212> DNA
 <213> Homo sapiens

 <400> 5
 ctggaaagac tccattcg 18

 <210> 6
 <211> 19
 <212> DNA
 <213> Homo sapiens

 <400> 6
 cacagaggcc tctcagaag 19

 <210> 7
 <211> 18
 <212> DNA
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 <400> 7
 ccccttcca tccgaatg 18

 <210> 8
 <211> 19
 <212> DNA
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 <400> 8
 gagctgctgt gtcgcagac 19

 <210> 9
 <211> 79
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> flag primer

 <400> 9
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 ggggcctgc agcggtcc 79

 <210> 10
 <211> 81
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> flag primer

<400> 10	
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gcccccttctt ggccccacga g	81
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<211> 31	
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<213> Homo sapiens	
<400> 11	
tatgcggccg ccaccatggg gccctgcagc g	31
<210> 12	
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<212> DNA	
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<400> 12	
tatgcggccg cgagctgctg tgcgcagac	30
<210> 13	
<211> 7	
<212> DNA	
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<400> 13	
rymaaya	7
<210> 14	
<211> 22	
<212> DNA	
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<400> 14	
tagtaaacac tctatcaatt gg	22
<210> 15	
<211> 20	
<212> DNA	
<213> Homo sapiens	
<400> 15	
gtccagtatc gtttacagcc	20
<210> 16	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 16	
cggatttgtt attggctgta c	21
<210> 17	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 17	
cggatttgtt atcggctgta c	21

<210> 18
 <211> 55
 <212> DNA
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<400> 18
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55

<210> 19
 <211> 518
 <212> PRT
 <213> Xenopus laevis

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 Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp
 20 25 30
 Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val
 35 40 45
 Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly
 50 55 60
 Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly
 65 70 75 80
 Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser
 85 90 95
 Met Ala Gly Asp His Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr
 100 105 110
 His Arg Tyr Tyr Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu
 115 120 125
 Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu
 130 135 140
 Lys Glu Val Ser Thr Leu Phe Pro Phe Asn Gly Asp Tyr Met Gly
 145 150 155 160
 Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys
 165 170 175
 Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp
 180 185 190
 Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn
 195 200 205
 Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala
 210 215 220
 Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr
 225 230 235 240
 Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu
 245 250 255
 Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met
 260 265 270
 Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala
 275 280 285
 Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn
 290 295 300
 Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr
 305 310 315 320
 Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser
 325 330 335
 Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys
 340 345 350
 Glu Gln Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile

[illegible]